

PCT10

RAW SEQUENCE LISTING DATE: 01/19/2002 PATENT APPLICATION: US/10/019,348 TIME: 11:38:41

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  3 <110> APPLICANT: Nelson, Peter S
          Hood, Leroy
          Lin, Biaoyang
  7 <120> TITLE OF INVENTION: Prostate-Specific Nucleic Acids
  9 <130> FILE REFERENCE: UOFW-1-18176
                                                                   ENTERED

✓ 11 <140> CURRENT APPLICATION NUMBER: US/10/019,348

12 <141> CURRENT FILING DATE: 2001-10-22
 14 <150> PRIOR APPLICATION NUMBER: PCT/US00/10920
 15 <151> PRIOR FILING DATE: 2000-04-21
 17 <150> PRIOR APPLICATION NUMBER: 60/130,778
 18 <151> PRIOR FILING DATE: 1999-04-23
 20 <150> PRIOR APPLICATION NUMBER: 60/151,585
 21 <151> PRIOR FILING DATE: 1999-08-30
 23 <150> PRIOR APPLICATION NUMBER: 60/174,003
 24 <151> PRIOR FILING DATE: 1999-12-30
 26 <150> PRIOR APPLICATION NUMBER: 60/177,751
 27 <151> PRIOR FILING DATE: 2000-01-24
 29 <160> NUMBER OF SEQ ID NOS: 42
 31 <170> SOFTWARE: PatentIn Ver. 2.0
 33 <210> SEQ ID NO: 1
 34 <211> LENGTH: 2538
 35 <212> TYPE: DNA
 36 <213> ORGANISM: Homo sapiens
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 39 <221> NAME/KEY: CDS
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 48 Pro Leu Leu Leu Leu Leu Pro Phe Leu Leu Tyr Met Ala Ala Pro
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 51 caa atc agg aaa atg ctg tcc agt ggg gtg tgt aca tca act gtt cag
 52 Gln Ile Arg Lys Met Leu Ser Ser Gly Val Cys Thr Ser Thr Val Gln
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 55 ctt cct ggg aaa gta gtt gtg gtc aca gga gct aat aca ggt atc ggg
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 56 Leu Pro Gly Lys Val Val Val Thr Gly Ala Asn Thr Gly Ile Gly
 59 aag gag aca gcc aaa gag ctg gct cag aga gga gct cga gta tat tta
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 60 Lys Glu Thr Ala Lys Glu Leu Ala Gln Arg Gly Ala Arg Val Tyr Leu
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                                         60
 63 gct tgc cgg gat gtg gaa aag ggg gaa ttg gtg gcc aaa gag atc cag
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64 Ala Cys Arg Asp Val Glu Lys Gly Glu Lew Val Ala Lys Glu Ile Gln 65 70 75 80 67 acc acq aca ggg aac cag cag ggt ttg gtg cgg aac ctg gac ctg tct 68 Thr Thr Gly Asn Gln Gln Val Lew Val Arg Lys Lew Asp Lew Ser 69 85 90 95 71 gat act aag tct att cga gct ttt gct aag ggc ttc tta gc gag gaa 72 Asp Thr Lys Ser Ile Arg Ala Phe Ala Lys Gly Phe Lew Ala Glu Glu 73 100 105 110 75 aag cac ctc cac gtt ttg atc aac aat gca gga gtg atg atg tgt ccg 76 Lys His Lew His Val Lew Ile Asn Asn Ala Gly Val Met Met Cys Pro 77 115 120 125 130 79 tac tcg aag aca gca gat ggc ttt gag atg cac ata gga gtc acc acc 490 80 Tyr Ser Lys Thr Ala Asp Gly Phe Glu Met His Ile Gly Val Asn His 11 135 140 145 83 ttg ggt cac ttc ctc cta acc cat ctg ctg cta gag aaa cta aag gaa 84 Lew Gly His Phe Lew Lew Thr His Lew Lew Glu Lys Lew Lys Glu 85 150 155 160 87 tca gcc cca tca agg atg atg aat gtc ttc cc gca cat cac ctg 88 Ser Ala Pro Ser Arg Ile Val Asn Val Ser Ser Lew Ala His His Lew 99 165 170 175 91 gga agg atc cac ttc cat aac ctg cag ggc gag aat tt tac aat gca 92 Gly Arg Ile His Phe His Asn Lew Gln Gly Glu Lys Phe Tyr Asn Ala 93 180 185 190 95 ggc ctg gcc tac tgt cac agc aag cta gcc aca tcc ctc ttc acc agc 96 Gly Lew Ala Tyr Cys His Ser Lys Lew Ala Asn Ile Lew Phe Thr Gln 195 200 205 99 gaa ctg gcc cgg aga cta acc gct ggc ggt tt acg acc ttc ttc acc 100 Glu Lew Ala Arg Arg Lew Lys Gly Ser Gly Val Thr Thr Tyr Ser Val 101 215 220 225 103 cac cct ggc aca gtc cac ttc tcc ttt tcc ttt ttc atc aat gcc 108 Arg Trp Met Trp Trp Lew Phe Ser Phe Phe Ile Lys Thr Pro Gln Gln 210 245 250 110 265 270 110 265 270 110 265 270 111 275 280 112 30 265 275 113 30 265 275 114 30 30 305 115 280 116 30 305 117 30 305 117 30 305 118 30 305 119 31 32 305 110 30																		
67 acc acg aca ggg aac cag cag ggg tgt ttg gtg cgg aaa ctg gac ctg tct 68 Thr Thr Thr Gly Asn Gln Gln Val Leu Val Arg Lys Leu Asp Leu Ser 69 95 97 71 gat act aag tct att cga gct ttt gat aag ggc ttc tta gct gag gaa 394 72 Asp Thr Lys Ser Ile Arg Ala Phe Ala Lys Gly Phe Leu Ala Glu Glu 73 100 105 110 75 aag cac ctc cac gtt ttg atc aac aat gca gga gtg atg atg gtg ccg 76 Lys His Leu His Val Leu Ile Asn Asn Ala Gly Val Met Met Cys Pro 77 115 120 125 130 79 tac tcg aag aca gca gat ggc ttt gag atg acc ata gga gtc acc acc 280 80 Tyr Ser Lys Thr Ala Asp Gly Phe Glu Met His Ile Gly Val Asn His 135 140 145 81 tug Ggt cac ttc ctc cta acc cat ctg ctg cta gag aaa cta aag gaa 84 Leu Gly His Phe Leu Leu Thr His Leu Leu Leu Glu Lys Leu Lys Glu 155 150 160 87 tca gcc cca tca agg ata gta at gtg tct tcc ctc gca cat cac ctg 88 Ser Ala Pro Ser Arg Ile Val Asn Val Ser Ser Leu Ala His His Leu 199 165 170 175 91 gga agg atc cac ttc cat aac ctg cag ggc gag aat tt tac aat gca 634 92 Gly Arg Ile His Phe His Asn Leu Gln Gly Glu Lys Phe Tyr Asn Ala 180 93 180 185 190 175 94 gga ctg gcc tag gcc tag aga cta aaa gcc agc act ctc ttc acc cag 66 Gly Leu Ala Tyr Cys His Ser Lys Leu Ala An Ile Leu Phe Thr Gln 97 195 200 205 210 95 gac ctg gcc cag aga cta aaa ggc tct ggc gtt acg acg tat tct ga 730 100 Glu Leu Ala Arg Arg Leu Lys Gly Ser Gly Val Thr Thr Tyr Ser Val 200 205 210 97 gaa ctg gcc cag acc aat ctc gaa ctg gct ggc act cat tct tta at 682 101 201 202 205 205 210 102 303 cac cct gga cac gtc caa tct gaa ctg gtc ttg gc cac tca tct ttc at 682 103 cac cct gga cac gtc caa tct gaa ctg gtc ttg gc gct tag act gct gcc ga gac cta acc gga gcc gag cta acc acc gag acc gtg cac tca tct ttc at 682 104 His Pro Gly Thr Val Gln Ser Glu Leu Val Arg His Ser Ser Phe Met 105 200 255 105 200 255 106 107 aga tgg att gg tgg ctt ttc tcc ttt tc acc aag act cct cag cag 62 108 Arg Trp Met Trp Trp Leu Phe Ser Phe Phe Ile Lys Thr Pro Gln Gln 205 255 109 109 100 Glu Leu Ala Arg Arg Leu Thr Slu Gly Leu Glu Ile 110 101 205 205 205 1020 205 207 1020 205 2		Ala	Cys	Arg	_	Val	Glu	Lys	Gly		Leu	Val	Ala	Lys		Ile	Gln	
88 Thr Thr Thr Gly Asn Gln Gln Val Leu Val Arg Lys Leu Asp Leu Ser 69 85 90 95 11 gat act aag tct att cga gct ttt gct aag ggc ttc tta gct gag gaa 394 12 Asp Thr Lys Ser Ile Arg Ala Phe Ala Lys Gly Phe Leu Ala Glu Glu 105 110 105 13 100 105 110 125 130 15 aag cac ctc cac gtt ttg atc aac aat gca gga gtg atg atg tgt ccg 442 16 Lys His Leu His Val Leu Ile Asn Asn Ala Gly Val Met Met Cys Pro 170 115 120 125 130 17 tac tcg aag aca gca gat ggc ttt gag atg cac ata gga gtc aac cac 680 Tyr Ser Lys Thr Ala Asp Gly Phe Glu Met His Ile Gly Val Asn His 11 135 140 145 18 ttg ggt cac ttc ctc cta acc cat ctg ctg cta gag aaa cta aag gaa 44 Leu Gly His Phe Leu Leu Thr His Leu Leu Glu Lys Leu Lys Glu 155 160 18 tca ggc cca tca agg ata gta aat gtg tct tcc ctc gca cat cac ctg 168 18 Ser Ala Pro Ser Arg Ile Val Asn Val Ser Ser Leu Ala His His Leu 165 170 175 19 gga agg atc cac ttc cat aac ctg gag gag aaa ttc ac aat gca 634 29 Gly Arg Ile His Phe His Asn Leu Glu Glu Lys Phe Tyr Asn Ala 185 190 19 gga agg atc cac ttc cat aac ctg cag ggc gag aaa ttc tac aat gca 634 29 Gly Arg Ile His Phe His Asn Leu Gln Gly Glu Lys Phe Tyr Asn Ala 193 180 185 190 20 gga ctg gcc tac tgt cac aga aag cta gc gc gag at tct ac act gca 64 20 Gly Leu Ala Tyr Cys His Ser Lys Leu Ala Asn Ile Leu Phe Thr Gln 200 205 20 gaa ctg gcc cgg aga cta aaa ggc tct ggc gtt acg acg tat tct gta 730 100 Glu Leu Ala Arg Arg Leu Lys Gly Ser Gly Val Thr Thr Tyr Ser Val 120 101 215 220 225 103 cac cct ggc aca gtc caa tct gaa ctg gtt cgg cac tca tct ttc atg 78 104 His Pro Gly Thr Val Gln Ser Glu Leu Val Arg His Ser Ser Phe Met 105 230 235 240 107 aga tgg atg tgg ctt ttc tc ttt tc act aca gaa ggt ctg agt gtg tt gg 25 111 gga gcc cag ca gc cag cac tg cac tgt gcc tgg gca tg agt gt gt 11 11 12 215 220 120 Cla Arg Trp Met Trp Trp Leu Phe Ser Phe Phe Hi Lys Thr Pro Gln Gln 255 111 gga gcc cag cag act act tc aga ctg tg tcg tg tg gct tg gg ctc tg ga ctg atg tg 11 11 12 215 220 120 Gln Ala Arg Asn Glu Thr Tle Ala Arg Arg Leu Trp Asp Val Ser Val 220 121 280 285 290																		246
90 95 71 gat act aatg tct att cgp gct ttt gct aag ggc ttc tta gct gag gaa 72 Asp Thr Lys Ser Ile Arg Ala Phe Ala Lys Gly Phe Leu Ala Glu Glu 73 100 105 110 75 aag cac ctc cac gtt ttg atc aac aat gca gga gtg atg atg tgt ccg 76 Lys His Leu His Val Leu Ile Asn Asn Ala Gly Val Met Met Cys Pro 77 115 120 125 130 79 tac tcg aag aca gca gat ggc ttt gag atg acc ata gga gtc aac cac 80 Tyr Ser Lys Thr Ala Asp Gly Phe Glu Met His Ile Gly Val Asn His 81 135 140 145 83 ttg ggt cac ttc ctc cta acc cat ctg ctg cta gag aaa cta aag gaa 84 Leu Gly His Phe Leu Leu Thr His Leu Leu Leu Glu Lys Leu Lys Glu 85 150 155 160 87 tca gcc cca tca agg ata gta atg tgt ccc 88 Ser Ala Pro Ser Arg Ile Val Asn Val Ser Ser Leu Ala His His Leu 91 165 170 91 gga agg atc cac ttc cat acc ctg cag ggc gag aaa ttc tac aat gca 92 Gly Arg Ile His Phe His Asn Leu Gln Gly Glu Lys Phe Tyr Asn Ala 93 180 185 190 95 ggc ctg gcc tac tgt cac agc aag cta gcc aac atc ctc ctc acc cag 96 Gly Leu Ala Tyr Cys His Ser Lys Leu Ala Asn Ile Leu Phe Thr Gln 97 195 200 205 210 99 gaa ctg gcc cgg aga cta aa ag gct ttg gg gtt acg att tct ga 100 Glu Leu Ala Arg Arg Leu Lys Gly Ser Gly Val Thr Thr Tyr Ser Val 101 215 220 225 103 cac cct ggc cag acc atc ttc cat tcg ac ctg gtt cgg cac tca tct tc atg 108 Arg Typ Met Trp Trp Leu Phe Ser Phe Ple ILe Lys Thr Pro Gln Gln 109 245 230 255 111 gga ccc cag acc agc ctg cac ttg tcc ttt tc acc aga agc cta ttc ttc acc ag cag 102 Agg atg dtg dtg ttg ctt ttc ctt tt acc aga agc ctc cag ag agc acc agc ctg cac tac acc ttc acc acc acc acc acc acc			_				-	_		_				_	-	_		346
71 gat act asg tct att cga gct ttt gct aag ggc ttc tta gct gag gaa		Thr	Thr		GTA	Asn	GIN	GIN		ьеи	vaı	Arg	ьуs		Asp	Leu	ser	
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73																		394
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85										_	_					_	_	330
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88 Ser Ala Pro Ser Arg Ile Val Asn Val Ser Ser Leu Ala His His Leu 89 165 170 175 91 gga agg atc cac ttc cat aac ctg cag ggc gag aaa ttc tac aat gca 634 92 Gly Arg Ile His Phe His Asn Leu Gln Gly Glu Lys Phe Tyr Asn Ala 93 180 185 190 95 ggc ctg gcc tac tgt cac agc aag cta gcc aac atc ctc ttc acc cag 682 96 Gly Leu Ala Tyr Cys His Ser Lys Leu Ala Asn Ile Leu Phe Thr Gln 97 195 200 205 210 99 gaa ctg gcc cgg aga cta aaa ggc tct ggc gtt acg acg tat tct gta 730 100 Glu Leu Ala Arg Arg Leu Lys Gly Ser Gly Val Thr Thr Tyr Ser Val 101 215 220 225 103 cac cct ggc aca gtc caa tct gaa ctg gtt gg cac tca tct ttc atg 778 104 His Pro Gly Thr Val Gln Ser Glu Leu Val Arg His Ser Ser Phe Met 105 230 235 240 107 aga tgg atg tgg tgg ctt ttc tcc ttt ttc atc aag act cct cag cag 826 108 Arg Trp Met Trp Trp Leu Phe Ser Phe Phe Ile Lys Thr Pro Gln Gln 109 245 250 255 111 gga gcc cag acc agc ctg cac tgt gcc tta aca gaa ggt ctt gag att 112 Gly Ala Gln Thr Ser Leu His Cys Ala Leu Thr Glu Gly Leu Glu Ile 113 260 265 270 115 cta agt ggg aat cat ttc agt gac tgt cat gtg gca ttg ggt tct gtc 922 116 Leu Ser Gly Asn His Phe Ser Asp Cys His Val Ala Trp Val Ser Val 117 275 280 285 290 119 caa gct cgt aat gag act ata gac agg ctg tgg gac gtc agt tgt 970 120 Gln Ala Arg Asn Glu Thr Ile Ala Arg Arg Leu Trp Asp Val Ser Cys 121 295 300 305 123 gac ctg ctg ggc ctc cca ata gac tacacaggcag tgccagttgg acccaagaga 1024 124 Asp Leu Leu Gly Leu Pro Ile Asp 125 310																		506
89			-					-						-			-	286
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92 Gly Arg Ile His Phe His Asn Leu Gln Gly Glu Lys Phe Tyr Asn Ala 93 180 185 190 95 ggc ctg gcc tac tgt cac agc aag cta gcc aac atc ctc ttc acc cag 682 96 Gly Leu Ala Tyr Cys His Ser Lys Leu Ala Asn Ile Leu Phe Thr Gln 97 195 200 205 210 99 gaa ctg gcc cgg aga cta aaa ggc tct ggc gtt acg acg tat tct gta 730 100 Glu Leu Ala Arg Arg Leu Lys Gly Ser Gly Val Thr Thr Tyr Ser Val 101 215 220 225 103 cac cct ggc aca gtc caa tct gaa ctg gtt cgg cac tca tct tc atg 778 104 His Pro Gly Thr Val Gln Ser Glu Leu Val Arg His Ser Ser Phe Met 105 230 235 240 107 aga tgg atg tgg tgg ctt ttc tcc ttt ttc atc aag act cct cag cag 826 108 Arg Trp Met Trp Trp Leu Phe Ser Phe Phe Ile Lys Thr Pro Gln Gln 109 245 250 255 111 gga gcc cag acc agc ctg cac tgt gcc tta aca gaa ggt ctt gag att 874 112 Gly Ala Gln Thr Ser Leu His Cys Ala Leu Thr Glu Gly Leu Glu Ile 113 260 265 115 cta agt ggg aat cat ttc agt gac tgt cat gtg gca tgg gtg tct gtc 922 116 Leu Ser Gly Asn His Phe Ser Asp Cys His Val Ala Trp Val Ser Val 117 275 280 285 290 119 caa gct cgt aat gag act ata gca agg cgg ctg tgg gac gtc agt tgt 970 120 Gln Ala Arg Asn Glu Thr Ile Ala Arg Arg Leu Trp Asp Val Ser Cys 121 295 300 305 123 gac ctg ctg ggc ctc cca ata gac tacaaaggcag tgccagttgg acccaaagga 1024 124 Asp Leu Leu Gly Leu Fro Ile Asp 125 310 127 agactgcagc agactacaca gtacttcttg tcaaaatgat tctccttcaa ggttttcaaa 1084																		
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96 Gly Leu Ala Tyr Cys His Ser Lys Leu Ala Asn Ile Leu Phe Thr Gln 97 195 200 205 210 99 gaa ctg gcc cgg aga cta aaa ggc tct ggc gtt acg acg tat tct gta 730 100 Glu Leu Ala Arg Arg Leu Lys Gly Ser Gly Val Thr Thr Tyr Ser Val 101 215 220 225 103 cac cct ggc aca gtc caa tct gaa ctg gtt cgg cac tca tct ttc atg 778 104 His Pro Gly Thr Val Gln Ser Glu Leu Val Arg His Ser Ser Phe Met 105 230 235 240 107 aga tgg atg tgg tgg ctt ttc tcc ttt ttc atc aag act cct cag cag 826 108 Arg Trp Met Trp Trp Leu Phe Ser Phe Phe Ile Lys Thr Pro Gln Gln 109 245 250 255 111 gga gcc cag acc agc ctg cac tgt gcc tta aca gaa ggt ctt gag att 874 112 Gly Ala Gln Thr Ser Leu His Cys Ala Leu Thr Glu Gly Leu Glu Ile 113 260 265 270 115 cta agt ggg aat cat ttc agt gac tgt cat gtg gca tgg gtg tct gtc 922 116 Leu Ser Gly Asn His Phe Ser Asp Cys His Val Ala Trp Val Ser Val 117 275 280 285 290 119 caa gct cgt aat gag act ata gca agg cgg ctg tgg gac gtc agt tgt 970 120 Gln Ala Arg Asn Glu Thr Ile Ala Arg Arg Leu Trp Asp Val Ser Cys 121 295 300 305 123 gac ctg ctg ggc ctc cca ata gac tacacagcag tgccagttgg acccaagaga 1024 124 Asp Leu Leu Gly Leu Pro Ile Asp 125 310 126 127 agactgcagc agactacaca gtacttcttg tcaaaatgat tctccttcaa ggttttcaaa 1084	93		180					185					190					
96 Gly Leu Ala Tyr Cys His Ser Lys Leu Ala Asn Ile Leu Phe Thr Gln 97 195 200 205 210 99 gaa ctg gcc cgg aga cta aaa ggc tct ggc gtt acg acg tat tct gta 730 100 Glu Leu Ala Arg Arg Leu Lys Gly Ser Gly Val Thr Thr Tyr Ser Val 101 215 220 225 103 cac cct ggc aca gtc caa tct gaa ctg gtt cgg cac tca tct ttc atg 778 104 His Pro Gly Thr Val Gln Ser Glu Leu Val Arg His Ser Ser Phe Met 105 230 235 240 107 aga tgg atg tgg tgg ctt ttc tcc ttt ttc atc aag act cct cag cag 826 108 Arg Trp Met Trp Trp Leu Phe Ser Phe Phe Ile Lys Thr Pro Gln Gln 109 245 250 255 111 gga gcc cag acc agc ctg cac tgt gcc tta aca gaa ggt ctt gag att 874 112 Gly Ala Gln Thr Ser Leu His Cys Ala Leu Thr Glu Gly Leu Glu Ile 113 260 265 270 115 cta agt ggg aat cat ttc agt gac tgt cat gtg gca tgg gtg tct gtc 922 116 Leu Ser Gly Asn His Phe Ser Asp Cys His Val Ala Trp Val Ser Val 117 275 280 285 290 119 caa gct cgt aat gag act ata gca agg cgg ctg tgg gac gtc agt tgt 970 120 Gln Ala Arg Asn Glu Thr Ile Ala Arg Arg Leu Trp Asp Val Ser Cys 121 295 300 305 123 gac ctg ctg ggc ctc cca ata gac tacacagcag tgccagttgg acccaagaga 1024 124 Asp Leu Leu Gly Leu Pro Ile Asp 125 310 126 127 agactgcagc agactacaca gtacttcttg tcaaaatgat tctccttcaa ggttttcaaa 1084	95	ggc	ctg	gcc	tac	tgt	cac	agc	aag	cta	gcc	aac	atc	ctc	ttc	acc	cag	682
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101						_						-	_	_			_	, , ,
103 cac cct ggc aca gtc caa tct gaa ctg gtt cgg cac tca tct ttc atg 778 104 His Pro Gly Thr Val Gln Ser Glu Leu Val Arg His Ser Ser Phe Met 105					9	_			, 017	DCI	_				-1-			
104 His Pro Gly Thr Val Gln Ser Glu Leu Val Arg His Ser Ser Phe Met 105			aat	· aac	, 202			tat		ata				, tca	tat			779
105																		770
107 aga tgg atg tgg tgg ctt ttc tcc ttt ttc atc aag act cct cag cag 108 Arg Trp Met Trp Trp Leu Phe Ser Phe Phe Ile Lys Thr Pro Gln Gln 109			PIC	, стх			GII	ı ser	GIU			. Aly	nrs	s ser			e Met	
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129 acctrtagea caaagagage aaaacettee ageettgeet gettggtgte cagttaaaac 1144																		
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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/019,348

DATE: 01/19/2002 TIME: 11:38:41

Input Set : A:\18176seq.txt

Output Set: N:\CRF3\01192002\J019348.raw

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196		50					55					60					
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DATE: 01/19/2002 RAW SEQUENCE LISTING PATENT APPLICATION: US/10/019,348 TIME: 11:38:41

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222	Asn	Ala	Gly	Leu	Ala	${ t Tyr}$	Cys		Ser	Lys	Leu	Ala		шe	Leu	Pne	
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229	225					230					235					240	
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232			_	_	245	-				250					255		
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238	0.2.0		275		1			280		-			285				
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241	DCI	290	0111		9		295				•	300		_	-		
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254 256 257 258 259	<22 <40 gtc	2> L0 0> S1 atat	OCATI EQUEI tga a	ION: NCE: acat	(57 3 tcca	ga ta	accta	atca [.]								Met 1	
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254 256 257 258 259 261 262	<22 <40 gtc. gct Ala	2> L0 0> S1 atat	OCAT: EQUEI tga a	ION: NCE: acat tca Ser	(57 3 tcca	ga ta	accta cca	atca [.] cca	gct Ala	att	gga	cct	tac	tat Tyr		Met 1 aac	
254 256 257 258 259 261 262 263	<22 <40 gtc gct Ala	2> L0 0> SI atat ttg Leu	OCATI EQUEI tga a aac Asn	ION: NCE: acat tca ser 5	(57 3 tcca ggg Gly	ga ta tca Ser	cca Pro	atca [.] cca Pro	gct Ala 10	att Ile	gga Gly	cct Pro	tac Tyr	tat Tyr 15	gaa Glu	Met 1 aac Asn	107
254 256 257 258 259 261 262 263 265	<22 <40 gtc. gct Ala	2> L0 0> S1 atat ttg Leu	OCAT: EQUEI tga a aac Asn	ION: NCE: acat tca Ser 5 caa	(57 3 tccae ggg Gly	ga ta tca Ser gaa	cca Pro	cca Pro	gct Ala 10 tat	att Ile	gga Gly gca	cct Pro	tac Tyr	tat Tyr 15	gaa Glu gtg	Met 1 aac Asn gtc	
254 256 257 258 259 261 262 263 265 266	<22 <40 gtc. gct Ala	2> L0 0> S1 atat ttg Leu	DCAT: EQUEI tga a aac Asn tac Tyr	ION: NCE: acat tca Ser 5 caa	(57 3 tccae ggg Gly	ga ta tca Ser gaa	cca Pro	cca Pro ccc Pro	gct Ala 10 tat	att Ile	gga Gly gca	cct Pro	tac Tyr ccc Pro	tat Tyr 15	gaa Glu	Met 1 aac Asn gtc	107
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254 256 257 258 259 261 262 263 265 266 267 269	<22 <40 gtc. gct Ala cat His	2> LG 0> SI atat ttg Leu gga Gly	aac Asn tac Tyr 20	tca Ser caa Gln	ggg Gly ccg Pro	tca Ser gaa Glu	cca Pro aac Asn	cca Pro ccc Pro 25	gct Ala 10 tat Tyr	att Ile ccc Pro	gga Gly gca Ala	cct Pro cag Gln	tac Tyr ccc Pro 30	tat Tyr 15 act Thr	gaa Glu gtg Val	Met 1 aac Asn gtc Val gtg	107
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254 256 257 258 259 261 262 263 265 266 267 269 270	<22 <40 gtc. gct Ala cat His ccc Pro	2> LOO 0> ST atat ttg Leu gga Gly act Thr	aac Asn tac Tyr 20 gtc Val	tca Ser caa Gln tac	(57 3 tccae ggg Gly ccg Pro gag Glu	tca Ser gaa Glu gtg Val	cca Pro aac Asn cat His	cca Pro ccc Pro 25 ccg	gct Ala 10 tat Tyr gct Ala	att Ile ccc Pro cag Gln	gga Gly gca Ala tac	cct Pro cag Gln tac Tyr 45	tac Tyr ccc Pro 30 ccg Pro	tat Tyr 15 act Thr tcc Ser	gaa Glu gtg Val ccc Pro	Met 1 aac Asn gtc Val gtg Val	107 155 203
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254 256 257 258 259 261 262 263 265 267 269 270 271 273	<22 <40 gtc. gct Ala cat His ccc Pro	2> LOO 0> ST atat ttg Leu gga Gly act Thr 35 cag	aac Asn tac Tyr 20 gtc Val	tca Ser caa Gln tac Tyr	(57 3 tccae ggg Gly ccg Pro gag Glu	tca Ser gaa Glu gtg Val	cca Pro aac Asn cat His 40	cca Pro ccc Pro 25 ccg Pro	gct Ala 10 tat Tyr gct Ala acg	att Ile ccc Pro cag Gln	gga Gly gca Ala tac Tyr	cct Pro cag Gln tac Tyr 45	tac Tyr ccc Pro 30 ccg Pro	tat Tyr 15 act Thr tcc Ser	gaa Glu gtg Val ccc Pro	Met 1 aac Asn gtc Val gtg Val gtc Val	107 155 203
254 256 257 258 259 261 262 263 265 267 270 271 273 274 275	<22 <40 gtc. gct Ala cat His ccc Pro	2> L0 0> Statatted ttg Leu gga Gly act Thr 35 cag Gln	aac Asn tac Tyr 20 gtc Val	tca Ser caa Gln tac Tyr	ggg Gly ccg Pro gag Glu ccg	tca Ser gaa Glu gtg Val agg Arg	cca Pro aac Asn cat His 40 gtc Val	cca Pro ccc Pro 25 ccg Pro ctg	gct Ala 10 tat Tyr gct Ala acg	att Ile ccc Pro cag Gln cag	gga Gly gca Ala tac Tyr gct Ala 60	cct Pro cag Gln tac Tyr 45 tcc Ser	tac Tyr ccc Pro 30 ccg Pro aac	tat Tyr 15 act Thr tcc Ser ccc	gaa Glu gtg Val ccc Pro gtc	Met 1 aac Asn gtc Val gtg Val gtc Val 65	107 155 203 251
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254 256 257 258 259 261 262 263 265 267 270 271 273 274 275 277 278	<22 <40 gtc. gct Ala cat His ccc Pro ccc Pro tgc Cys	2> L(0) S) atat ttg Leu gga Gly act Thr 35 cag Gln acg	aac Asn tac Tyr 20 gtc Val tac Tyr	tca ser caa Gln tac Tyr gcc Ala	ggg Gly ccg Pro gag Glu ccg Pro aaa Lys	tca Ser gaa Glu gtg Val agg Arg 55 tcc Ser	cca Pro aac Asn cat His 40 gtc Val cca	cca Pro ccc Pro 25 ccg Pro ctg Leu	gct Ala 10 tat Tyr gct Ala acg Thr	att Ile ccc Pro cag Gln cag Gln aca Thr	gga Gly gca Ala tac Tyr gct Ala 60 gtg Val	cct Pro cag Gln tac Tyr 45 tcc Ser tgc Cys	tac Tyr ccc Pro 30 ccg Pro aac Asn	tat Tyr 15 act Thr tcc Ser ccc Pro	gaa Glu gtg Val ccc Pro gtc Val aag Lys 80	Met 1 aac Asn gtc Val gtg Val 65 act Thr	107 155 203 251
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254 256 257 258 259 261 262 263 265 267 270 271 273 274 275 277 278 279	<22 <40 gtc. gct Ala cat His ccc Pro ccc Pro tgc Cys	2> L(0) S) atat ttg Leu gga Gly act Thr 35 cag Gln acg Thr	aac Asn tac Tyr 20 gtc Val tac Tyr cag Gln gca	tca Ser Scaa Gln tac Tyr gcc Ala ccc Pro	ggg Gly ccg Pro gag Glu ccg Pro aaa Lys 70 tgc	tca Ser gaa Glu gtg Val agg Arg 55 tcc Ser	cca Pro aac Asn cat His 40 gtc Val cca Pro	cca Pro ccc Pro 25 ccg Pro ctg Leu tcc Ser	gct Ala 10 tat Tyr gct Ala acg Thr ggg Gly acc	att Ile ccc Pro cag Gln cag Gln aca Thr 75	gga Gly gca Ala tac Tyr gct Ala 60 gtg Val	cct Pro cag Gln tac Tyr 45 tcc Ser tgc Cys	tac Tyr ccc Pro 30 ccg Pro aac Asn acc	tat Tyr 15 act Thr tcc Ser ccc Pro	gaa Glu gtg Val ccc Pro gtc Val aag Lys 80 gtg	Met 1 aac Asn gtc Val gtg Val 65 act Thr	107 155 203 251 299
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RAW SEQUENCE LISTING DATE: 01/19/2002 PATENT APPLICATION: US/10/019,348 TIME: 11:38:41

Input Set : A:\18176seq.txt

Output Set: N:\CRF3\01192002\J019348.raw

285	gct	gcg	ctg	gcc	gct	ggc	cta	ctc	tgg	aag	ttc	atg	ggc	agc	aag	tgc	395
286	Ala	Ala	Leu	Ala	Ala	Gly	Leu	Leu	Trp	Lys	Phe	Met	Gly	Ser	Lys	Cys	
287			100					105					110				
289	tcc	aac	tct	ggg	ata	gag	tgc	gac	tcc	tca	ggt	acc	tgc	atc	aac	CCC	443
290	Ser	Asn	Ser	Gly	Ile	Glu	Cys	Asp	Ser	Ser	Gly	Thr	Cys	Ile	Asn	Pro	
291		115					120					125					
293	tct	aac	tgg	tgt	gat	ggc	gtg	tca	cac	tgc	CCC	ggc	ggg	gag	gac	gag	491
294	Ser	Asn	${\tt Trp}$	Cys	Asp	Gly	Val	Ser	His	Cys	Pro	Gly	Gly	Glu	Asp		
295						135					140	,				145	
297	aat	cgg	tgt	gtt	cgc	ctc	tac	gga	cca	aac	ttc	atc	ctt	cag	atg	tac	539
	Asn	Arg	Cys	Val		Leu	Tyr	Gly	Pro		Phe	Ile	Leu	GIn	Met	Tyr	
299					150					155					160		507
301	tca	tct	cag	agg	aag	tcc	tgg	cac	cct	gtg	tgc	caa	gac	gac	tgg	aac	587
	Ser	Ser	Gln		Lys	Ser	Trp	His		Val	Cys	GIn	Asp		Trp	Asn	
303				165					170					175			625
305	gag	aac	tac	ggg	cgg	gcg	gcc	tgc	agg	gac	atg	gge	Tat	aag	aat	dd L Aan	635
	GIu	Asn		GLY	Arg	Ala	Ala		Arg	Asp	мет	GLY		ьуs	Asn	ASII	
307			180					185				~ ~ ~	190	200	200	+++	683
309	ttt	tac	tct	agc	caa	gga	ata	gtg	gat	gac	age	gga	Cor	acc mb∞	agc	Dho	003
	Phe	_	ser	ser	GIN	GTA		vaı	ASP	Asp	ser	205	ser	THI	Ser	PHE	
311		195				- ~+	200	~~~	2 2 ±	a+a	ant.		+ > +	222	222	ata	731
313	Mot	aaa Ta	Tou	Aan	Thr	cor	N la	Gl ₁₇	Aar Aan	Val	Agn	Tle	Tur	Lvs	aaa Lys	Len	731
314		ьуѕ	Leu	ASII	1111	215	ніа	GIY	ASII	Vai	220	116	тут	цуз	цуз	225	
		020	ant	ast	acc	_	tot	toa	aaa	aca		att	tct	tta	cgc		779
31Q	Tur	Uie	Ser	yat Aen	Δla	Cve	Ser	Ser	Lvs	Ala	Val	Val	Ser	Leu	Arg	Cvs	
319	тут	1113	DCI	изъ	230	Cys	DCI	DCI	-15	235	,	,	202		240	-1-	
	tta	acc	tac	aaa		aac	t.t.a	aac	t.ca		cac	caq	agc	agg	atc	ata	827
322	Leu	Ala	Cvs	Glv	Val	Asn	Leu	Asn	Ser	Ser	Arg	Gln	ser	Arg	Ile	Val	
323			- 1 -	245					250					255			
	aac	qqt	qaq	agc	qcq	ctc	ccq	qqq	gcc	tgg	ccc	tgg	cag	gtc	agc	ctg	875
326	Gly	Gly	Glu	Ser	Ala	Leu	Pro	Gly	Ala	Trp	Pro	Trp	Gln	Val	Ser	Leu	
327	•	-	260					265					270				
329	cac	gtc	cag	aac	gtc	cac	gtg	tgc	gga	ggc	tcc	atc	atc	acc	CCC	gag	923
330	His	Va1	Gln	Asn	Val	His	Val	Cys	Gly	Gly	Ser	Ile	Ile	Thr	Pro	Glu	
331		275					280					285					
333	tgg	atc	gtg	aca	gcc	gcc	cac	tgc	gtg	gaa	aaa	cct	ctt	aac	aat	cca	971
334	Trp	Ile	Val	Thr	Ala	Ala	His	Cys	Val	Glu	Lys	Pro	Leu	Asn	Asn	Pro	
	290					295					300					305	
337	tgg	cat	tgg	acg	gca	ttt	gcg	ggg	att	ttg	aga	caa	tct	ttc	atg	ttc	1019
338	Trp	His	Trp	Thr	Ala	Phe	Ala	Gly	Ile		Arg	Gln	Ser	Phe	Met	Phe	
339					310					315					320		
341	tat	gga	gcc	gga	tac	caa	gta	caa	aaa	gtg	att	tct	cat	cca	aat	tat	1067
	Tyr	Gly	Ala	Gly	Tyr	Gln	Val	Gln		Val	Ile	Ser	His		Asn	Tyr	
343				325					330					335			
345	gac	tcc	aag	acc	aag	aac	aat	gac	att	gcg	ctg	atg	aag	ctg	cag	aag	1115
	Asp	Ser		Thr	Lys	Asn	Asn		Ile	Ala	Leu	Met		Leu	Gln	ràs	
347	_		340					345				. .	350			222	1160
349	cct	ctg	act	ttc	aac	gac	cta	gtg	aaa	cca	gtg	tgt	ctg	ccc	aac	cca	1163

Use of n and/or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

DATE: 01/19/2002

PATENT APPLICATION: US/10/019,348

TIME: 11:38:42

Input Set : A:\18176seq.txt

Output Set: N:\CRF3\01192002\J019348.raw

L:11 M:270 C: Current Application Number differs, Replaced Application Number

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:702 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1564 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1584 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:1676 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20